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RAW SEQUENCE LISTING

DATE: 02/24/2002

PATENT APPLICATION: US/10/054,691

TIME: 15:31:36

Input Set : N:\Crf3\Refhold\J054691.raw

Output Set: N:\CRF3\02222002\J054691.raw

ENTERED

1 <110> APPLICANT: Yu, Xuanchuan
 2 Miranda Maricar
 3 Turner, C. Alexander Jr.
 4 <120> TITLE OF INVENTION: Novel Human Lipase and Polynucleotides Encoding the Same
 5 <130> FILE REFERENCE: LEX-0303-USA
 6 <140> CURRENT APPLICATION NUMBER: US/10/054,691
 7 <141> CURRENT FILING DATE: 2001-01-22
 8 <150> PRIOR APPLICATION NUMBER: US 60/264,049
 9 <151> PRIOR FILING DATE: 2001-01-24
 10 <160> NUMBER OF SEQ ID NOS: 2
 11 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 4377
 14 <212> TYPE: DNA
 15 <213> ORGANISM: homo sapiens
 16 <400> SEQUENCE: 1

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18      ctgaagaatt ctccattccc atgcaaccca aataaattag gagtgaatat gccttctaaa 180
19      ttagttcaat ctctgaaacc ttctgatatt aaatttctgg cagccattgg caattctgaa 240
20      attctctcag acccagggac gggcgatctg gagaagcaag actggactga aaggccacag 300
21      caggtgtgca tgggagtjat jacagtcttt tcajacatca tcagatattt cagtctctct 360
22      gtctcaatgc ctgtgtgcca cactggaaa agagtcatat cccacgatgg tctgaagac 420
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25      cctctctctc aacagaaatg gcttggggcg ggcggctgg atgagctgat gggggtgctg 600
26      gactacctgc agcaggajjt cccagagaca ttctataacc tgggtggact ctctgaggtt 660
27      gcagaggtct ctgttcagta tcaaggcaat tggctcagcc ctgcaccaga gacctgtaat 720
28      tctcagaggg agaccacccg gctggccaa gttgttatgc agtgggttta tcaggagacc 780
29      tggaaacagc tcttggtctc cagcaggtac agtcaagcag actccttcaa ctgtgttttc 840
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41      aaagactgga agataataac cctgtttata gggggcaatg acctctgtga ttctgcaat 1560
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47      tctccctgtg tcttgaagtt tcatgataac tcacagagac ttgctaccc tctcgaattc 1800
48      aacaaagagt ttccagagaa gcccacccaa ctgattgaga ttggtgagaa tgacacaaag 1860
49      gaagatttta ctgtgtttgt gcagccgttc ttgaaaaag ttgacatgac aaagacctct 1920
50      gaaggattgc ctgacaactc ttctctcctc cctgactgtt tccacttcag cagcaagttc 1980
51      cactcccgag cagccagctc tctctgggac aatatgtctg agcctgttgg ccagaaagag 2040
52      actcgtcata agtttgaaaa caagatccat atccatgttc cgaacccaggt ccagccgttt 2100
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70      cccactcaga atgagccctt cctgagaaac cctcgggaata gtaactaac gtaccccact 3180
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91 <210> SEQ ID NO: 2

92 <211> LENGTH: 1458

93 <212> TYPE: PRT

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95 <213> ORGANISM: homo sapiens

96 <400> SEQUENCE: 2

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100 20 25 30
101 Glu Gly Gln Leu Trp Pro Glu Thr Leu Lys Asn Ser Pro Phe Pro Cys
102 35 40 45
103 Asn Pro Asn Lys Leu Gly Val Asn Met Pro Ser Lys Ser Val His Ser
104 50 55 60
105 Leu Lys Pro Ser Asp Ile Lys Phe Val Ala Ala Ile Gly Asn Leu Glu
106 65 70 75 80
107 Ile Pro Pro Asp Pro Gly Thr Gly Asp Leu Glu Lys Gln Asp Thr Thr
108 85 90 95
109 Glu Arg Pro Gln Gln Val Cys Met Gly Val Met Thr Val Leu Ser Asp
110 100 105 110
111 Ile Ile Arg Tyr Phe Ser Pro Ser Val Pro Met Pro Val Cys His Thr
112 115 120 125
113 Gly Lys Arg Val Ile Pro His Asp Gly Ala Glu Asp Leu Trp Ile Gln
114 130 135 140
115 Ala Gln Glu Leu Val Arg Asn Met Lys Glu Asn Leu Gln Leu Asp Phe
116 145 150 155 160
117 Gln Phe Asp Trp Lys Leu Ile Asn Val Phe Phe Ser Asn Ala Ser Gln
118 165 170 175
119 Cys Tyr Leu Cys Pro Ser Ala Gln Gln Asn Gly Leu Ala Ala Gly Gly
120 180 185 190
121 Val Asp Glu Leu Met Gly Val Leu Asp Tyr Leu Gln Gln Gln Val Pro
122 195 200 205
123 Arg Ala Phe Val Asn Leu Val Asp Leu Ser Glu Val Ala Glu Val Ser
124 210 215 220
125 Arg Gln Tyr His Gly Thr Trp Leu Ser Pro Ala Pro Glu Pro Cys Asn
126 225 230 235 240
127 Cys Ser Glu Glu Thr Thr Arg Leu Ala Lys Val Val Met Gln Trp Ser
128 245 250 255
129 Tyr Gln Glu Ala Trp Asn Ser Leu Leu Ala Ser Ser Arg Tyr Ser Glu
130 260 265 270
131 Gln Gln Ser Phe Thr Val Val Phe Gln Pro Phe Phe Tyr Glu Thr Thr
132 275 280 285
133 Pro Ser Leu His Ser Glu Asp Pro Arg Leu Gln Asp Ser Thr Thr Leu
134 290 295 300
135 Ala Trp His Leu Trp Asn Arg Met Met Glu Pro Ala Gly Glu Lys Asp
136 305 310 315 320
137 Gln Pro Leu Ser Val Lys His Gly Arg Pro Met Lys Cys Pro Ser Gln
138 325 330 335
139 Gln Ser Pro Tyr Leu Phe Ser Tyr Arg Asn Ser Asn Tyr Leu Thr Arg
140 340 345 350
141 Leu Gln Lys Pro Gln Asp Lys Leu Glu Val Arg Glu Gly Ala Glu Ile
142 355 360 365
143 Arg Cys Pro Asp Lys Asp Pro Ser Asp Thr Val Pro Thr Ser Val His

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144	370	375	380
145	Arg Leu Lys Pro Ala Asp Ile Asn Val Ile Gly Ala Leu Gly Asp Ser		
146	385	390	395
147	Leu Thr Ala Gly Asn Gly Ala Gly Ser Thr Pro Gly Asn Val Leu Asp		
148		405	410
149	Val Leu Thr Gln Tyr Arg Gly Leu Ser Trp Ser Val Gly Gly Asp Glu		
150		420	425
151	Asn Ile Gly Thr Val Thr Thr Leu Ala Asn Ile Leu Arg Gln Phe Asn		
152		435	440
153	Pro Ser Leu Lys Gly Phe Ser Val Gly Thr Gly Lys Gln Thr Ser Pro		
154		450	455
155	Asn Ala Phe Leu Asn Gln Ala Val Ala Gly Gly Arg Ala Gln Asp Leu		
156		465	470
157	Pro Val Gln Ala Arg Arg Leu Val Asp Leu Met Lys Asn Asp Thr Arg		
158		485	490
159	Ile His Phe Gln Gln Asp Trp Lys Ile Ile Thr Leu Phe Ile Gly Gly		
160		500	505
161	Asn Asp Leu Cys Asp Phe Cys Asn Asp Leu Val His Tyr Ser Pro Gln		
162		515	520
163	Asn Phe Thr Asp Asn Ile Gly Lys Ala Leu Asp Ile Leu His Ala Glu		
164		530	535
165	Val Pro Arg Ala Phe Val Asn Leu Val Thr Val Leu Gln Ile Val Asn		
166		545	550
167	Leu Arg Gln Leu Tyr Gln Gln Lys Lys Val Tyr Cys Pro Arg Met Ile		
168		565	570
169	Leu Arg Ser Leu Cys Pro Cys Val Leu Lys Phe Asp Asp Asn Ser Thr		
170		580	585
171	Glu Leu Ala Thr Leu Ile Gln Phe Asn Lys Lys Phe Gln Gln Lys Thr		
172		595	600
173	His Gln Leu Ile Gln Ser Gly Arg Tyr Asp Thr Arg Gln Asp Phe Thr		
174		610	615
175	Val Val Val Gln Pro Phe Phe Gln Asn Val Asp Met Pro Lys Thr Ser		
176		625	630
177	Glu Gly Leu Pro Asp Asn Ser Phe Phe Ala Pro Asp Cys Phe His Phe		
178		645	650
179	Ser Ser Lys Ser His Ser Arg Ala Ala Ser Ala Leu Trp Asn Asn Met		
180		660	665
181	Leu Gln Pro Val Gly Gln Lys Thr Thr Arg His Lys Phe Gln Asn Lys		
182		675	680
183	Ile Asn Ile Thr Cys Pro Asn Gln Val Gln Pro Phe Leu Arg Thr Tyr		
184		690	695
185	Lys Asn Ser Met Gln Gly His Gly Thr Trp Leu Pro Cys Arg Asp Arg		
186		705	710
187	Ala Pro Ser Ala Leu His Pro Thr Ser Val His Ala Leu Arg Pro Ala		
188		725	730
189	Asp Ile Gln Val Val Ala Ala Leu Gly Asp Ser Leu Thr Ala Gly Asn		
190		740	745
191	Gly Ile Gly Ser Lys Pro Asp Asp Leu Pro Asp Val Thr Thr Gln Tyr		
192		755	760

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193 Arg Gly Leu Ser Tyr Ser Ala Gly Gly Asp Gly Ser Leu Glu Asn Val
194 770 775 780
195 Thr Thr Leu Pro Asn Ile Leu Arg Glu Phe Asn Arg Asn Leu Thr Gly
196 785 790 795 800
197 Tyr Ala Val Gly Thr Gly Asp Ala Asn Asp Thr Asn Ala Phe Leu Asn
198 805 810 815
199 Gln Ala Val Pro Gly Ala Lys Ala Glu Asp Leu Met Ser Glu Val Gln
200 820 825 830
201 Thr Leu Met Gln Lys Met Lys Asp Asp His Arg Val Asn Phe His Glu
202 835 840 845
203 Asp Trp Lys Val Ile Thr Val Leu Ile Gly Gly Ser Asp Leu Cys Asp
204 850 855 860
205 Tyr Cys Thr Asp Ser Asn Leu Tyr Ser Ala Ala Asn Phe Val Asp His
206 865 870 875 880
207 Leu Arg Asn Ala Leu Asp Val Leu His Arg Glu Val Pro Arg Val Leu
208 885 890 895
209 Val Asn Leu Val Asp Phe Leu Asn Pro Thr Ile Met Arg Gln Val Phe
210 900 905 910
211 Leu Gly Asn Pro Asp Lys Cys Pro Val Gln Gln Ala Ser Val Leu Cys
212 915 920 925
213 Asn Cys Val Leu Thr Leu Arg Glu Asn Ser Gln Glu Leu Ala Arg Leu
214 930 935 940
215 Glu Ala Phe Ser Arg Ala Tyr Arg Ser Ser Met Arg Glu Leu Val Gly
216 945 950 955 960
217 Ser Gly Arg Tyr Asp Thr Gln Glu Asp Phe Ser Val Val Leu Gln Pro
218 965 970 975
219 Phe Phe Gln Asn Ile Gln Leu Pro Val Leu Ala Asp Gly Leu Pro Asp
220 980 985 990
221 Thr Ser Phe Phe Ala Pro Asp Cys Ile His Pro Asn Gln Lys Phe His
222 995 1000 1005
223 Ser Gln Leu Ala Arg Ala Leu Trp Thr Asn Met Leu Glu Pro Leu Gly
224 1010 1015 1020
225 Ser Lys Thr Glu Thr Leu Asp Leu Arg Ala Glu Met Pro Ile Thr Cys
226 1025 1030 1035 1040
227 Pro Thr Gln Asn Glu Pro Phe Leu Arg Thr Pro Arg Asn Ser Asn Tyr
228 1045 1050 1055
229 Thr Tyr Pro Ile Lys Pro Ala Ile Glu Asn Trp Gly Ser Asp Phe Leu
230 1060 1065 1070
231 Cys Thr Gln Trp Lys Ala Ser Asn Ser Val Pro Thr Ser Val His Gln
232 1075 1080 1085
233 Leu Arg Pro Ala Asp Ile Lys Val Val Ala Ala Leu Gly Asp Ser Leu
234 1090 1095 1100
235 Thr Thr Ala Val Gly Ala Arg Pro Asn Asn Ser Ser Asp Leu Pro Thr
236 1105 1110 1115 1120
237 Ser Trp Arg Gly Leu Ser Trp Ser Ile Gly Gly Asp Gly Asn Leu Glu
238 1125 1130 1135
239 Thr His Thr Thr Leu Pro Asn Ile Leu Lys Lys Phe Asn Pro Tyr Leu
240 1140 1145 1150
241 Leu Gly Phe Ser Thr Ser Thr Trp Glu Gly Thr Ala Gly Leu Asn Val

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VERIFICATION SUMMARY

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